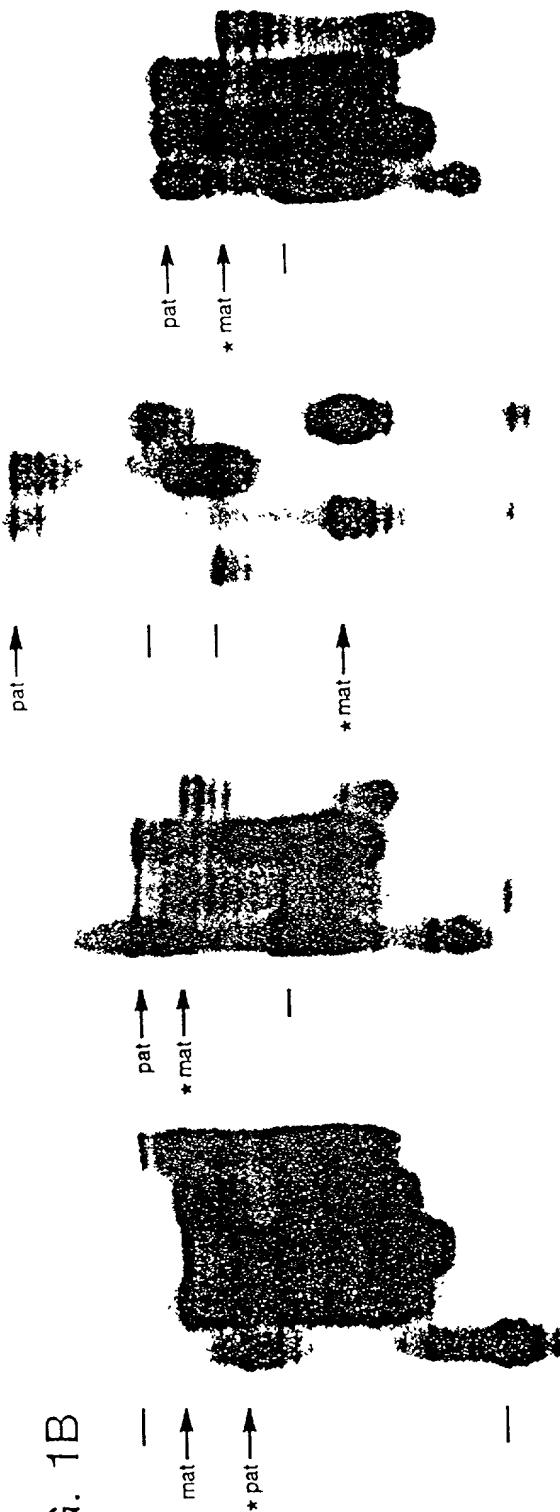


FIG. 1A

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D15S127 PF ph P¹ PM PF ph P¹ PM PF ph P¹ PM PF ph P¹ PM

FIG. 1B



ggcggccggcgtggatccggggaaatggatccctggccggcttaggatctcggtgcaggattatggct 80
 GCTGTTCTCAAAATAATCTACAGGAGCAACTAGAACCGTCACTCAGCCAGAACACTTAATAATTAAAGTCTTCAAA 160
 3 A V P Q N N L Q E Q L E R H S A R T L N N K L S L S K M A
 ACCAAAATTTCAGGTTTCACTTTAAAGAAAACATCTTCAGATAACATGTATCTGTAACTAATGTGTCACTAGCAA 240
 30 P K F S G F T F K K T S S D N N V S V T N V S V A
 AAAACACCTGTATTAAAGAATAAAAGATGTAAATGTTAACCGGAAGACTTTCCTTCAGTGAACTCTACCCAAACACCACAAAT 320
 56 K T P V L R N K D V N V T E D F S F S E P L P N T T N
 CAGCAAAGGGTCAAGGACTTCTTAAAAATGCTCCAGGAGCACGAAACACAGAGGTGGATCAAATCATTATTGCC 400
 83 Q Q R V K D F F K N A P A G Q E T Q O R G G S K S L L P
 AGATTTCTTGAGACTCCGAAGGAAGTGTATGCACTACCAAAACACCAACTGTAAGAAATCCGGATACTGCTC 480
 110 D F L Q T P K E V V C T T Q N T P T V K K S R D T A
 TCAAGAAATTAGAATTAGTTCACCGAGTTCTTAAAGTACCATCAATGATGGATGATGGATGACTTTGATACT 560
 135 L K K L E F S S P D S L S T I N D W D D M D D F D T
 TCTGAGACTTCAAATCATTGTTACACCACCCCAAGTCACTTGTAAAGAGTAAGCCACTGCTCAGAAATCAGAAAAGGG 640
 163 S E T S K S F V T P P Q S H F V R V S T A Q K S K K G
 TAAGAGAAACTTTAAAGCACACAGTTATAACAACACAGTAAGACTGATTGCTCCACCCCTCTGAAAGCG 720
 190 K R N F F K A Q L Y T T N T V K T D L P P S S E S
 AGCAAAATAGATTGACTGAGGAAACAGAAAGGATGACTCAGAATGGTTAACCGAGGGATGTTGATGATGATGCC 800
 216 E Q I D L T E E Q K D D S E W L S S D V I C I D D G P
 ATTGCTGAAGTGCATAATAATGAGATGCTCAGGAAAGTCACTCTGAAACTCATTTGGAAAGATGAAAGAGATAATAG 880
 243 I A E V H I N E D A Q E S D S L K T H L E D E R D N S
 CGAAAGACATGAAAGATTGGAAGAGCTGAAATTACATTCAACTGAGAAAGTTCACATGATTGATGATGATT 960
 270 E K K K N L E E A E L H S T E K V P C I E F D D D
 ATGATAACGGATTGTTGCTCACCTTCAGAAATTATTTCGCTTCTTCCTTCAAAATGCCATTAGTACGTTA 1040
 296 Y D T D F V P S P E E I I S A S S S K C L S T L
 AACGACCTTGACACATCTGACAGAAAAGAGATCTTGTCAAAAGATCTTGTCAAAACCTGAGAAAATGAG 1120

FIG. 2A

FIG. 2B

696 S L C Y Q L P A C V S P G V T V V I S P L R S L I V D
 CAAGTCCAAAGCTGACTTCCTGGATATTCCAGCTACATATCTG
CACGGTGATAAGACTGACTCAGAAGCTACAATAAT 2320
 723 Q V Q K L T S L D I P A T Y L T G D K T D S E A T N I
 TTACCTCCAGTTATCAAAAAGACCAATCATAAAACCTCTATATGTCACTCCAGAAAAGATCTGTGCAAGTAACGAC 2400
 750 Y L Q L S K K D P I I K L L Y V T P E K I C A S N R
 TCATTCTACTCTGGAGAATCTATGAGGGAAAGCTCTGGCACGTTTGTATTGATGAAGCACATTGTGTCACTCAG 2480
 776 L I S T L E N L Y E R K L L A R F V I D E A H C V S Q
 TGGGACATGATTTCGTCAGATTACAAAGAATGAAATGCTTCGCCAGGAAAGTTCCCGTGTGATGGCTCT 2560
 803 W G H D F R Q D Y K R M N M L R Q K F P S V P V M A L
 TACGGCCACAGCTAAATCCAGGTACAGAACGACTCTG
ACTCAGCTGACATCTGAGATCTCAGACCTCAGGGTGTGTTAGCATGA 2640
 830 T A T A N P R V Q K D I L T Q L K I L R P Q V F S M
 GCTTAACAGACATAATCTGAAATACTATGTTACCCAAAAAGCTAAAGGCTAAAGGCTAAAGGCTAAATGGATC 2720
 856 S F N R H N L K Y V L P K K P K V A F D C L E W I
 AGAAAGCACCACCATATGATTCAAGGCTAAATTACTGCCTCTCCAGGCTCAGTGTGAACTGGCTGACACCGTTACA 2800
 883 R K H H P Y D S G I I Y C L S R R E C D T M A D T L Q
 GAGAGATGGCTCGCTGCTCTGGCTTACCATGCTGGCTCAGTGTGAACTGGCTCAGGAGATGAGTGGGATTA 2880
 910 R D G L A A L A Y H A G L S D S A R D E V Q Q K W I
 ATCAGGATGGCTGTCAGGTTATCTGTGGCTACAAATTGCAATTGGATGGGATTGACAAACCCGACGTGGGATTGGATT 2960
 936 N Q D G C Q V I C A T I A F G M G I D K P D V R F V I
 CATGCATCTCCCTAAATCTGTGAGGGTTACTACCAAGAATCTGGCAGGCTGGAAAGAGATGGGAAATATCTCACTG 3040
 963 H A S L P K S V E G Y Y Q E S G R A G R D G E I S H C
 CCTGGCTTCTATACCDATCATGATGTGACCCAGACTGAAAGACTTATAATGATGGAAAAGATGGAAACCATCATACAA 3120
 990 L L F Y T Y H D V T R L K R L I M M E K D G N H H T
 GAGAAACTCACTCAATAATTGATAGGATGGTACATTACTGTGAAAATATAACCGGAATGCCAGGAGAATACAGCTTTTG 3200
 1016 R E T H F N N L Y S M V H Y C E N I T E C R R I Q L L
 GCCTACTTTGGTGAATGGATTAACTCTGATTCTGATTCTGATAATTGCTGATAATTGCTGTAAAC 3280
 1043 A Y F G E N G F N P D F C K K H P D V S C D N C C K T

FIG. 2C

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FIG. 2D

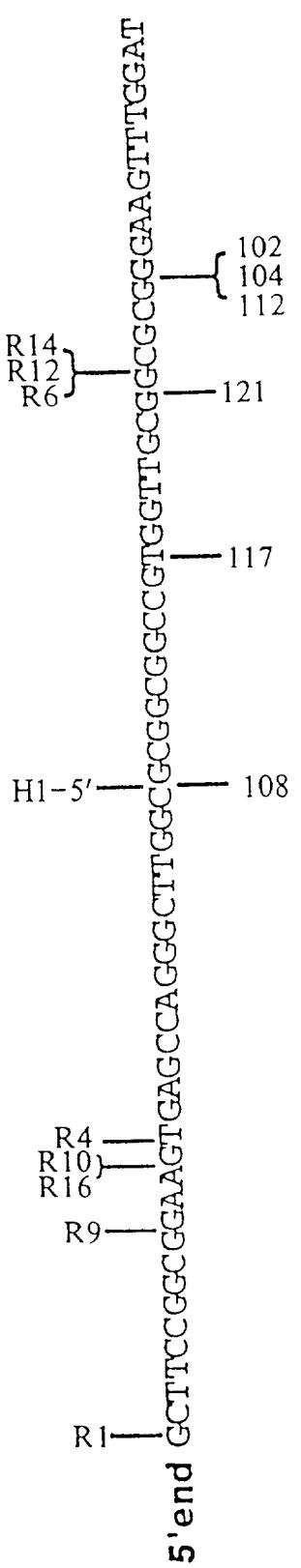


FIG. 3

* I F PHTKEMMKI FHKKGFLHNFRTNQLEA IN A ALLGCFILMPTGGGKSLCYOLPACV---SPGVTVVISPLRSLIVDQV BLM
 649 FPWSGKVKDII LQNVFKLEKFRPLQLETINVTMAGKEVFVLMPTGGGKSLCYOLPALC---SDGFTLVICPLISLME DQL REQL
 74 YPW SDEVLYRHLHEVFKLPGFRPNQLEAVNATLQGKDFVFLMPGGGKSLCYOLPAVVKSGKTHGTTIVISPLISLMDQV SGS1
 659 --- VLTQETFGYQQFRPGQEEI IDTVLSCRDCLVVMPGGGKSLCYQIPALL---LNGLT VVVSPPLISLMDQV recQ
 16

* Ia QKLTSLDIPATYLTDSEATNIYLQLSKKDP I KLLYVTPEKICASNRLLISTLENLYERKLLARFVIDEAHCVSQWG BLM
 725 MVLKOLGISA TMINASSSKEHVKWVHD EMVNKNSELKLIYVTPEKIAKS KMFMSRLEKAYEARRFTRIAVDEVHCCSQWQ REQL
 150 EHLLNKNIKASMFS SSRGTAEQRRTENLFIN---GLLDDLVYISPEMISASEQCKRAISRLYADGKLAR IIVDVAEHCVSNTWG SGS1
 739 DQLQANGVA AA CLNSTQTREQQLEVM T---GCRTGQIRRLLYA PERL---MLDNFLEHL-AHWNPNVLLAVDEAHCISQWG recQ
 83

* II HD FRQDYKRMNMLRQKFPSVPV MALTATANPRVQKDILTQLKILRPQVFSMSFN RHNLKYYVLPKKVVA---FDCLEW BLM
 805 H DFRPDYKALGILK RQFPNASLIGLTATA TNHVLTD AQKILCIEKCF FTASFN RPNL---YEV RQKP SNTEDFIEDIVKL REQL
 230 H DFRPDYKELKF KREYPDIPMIALTATA SEQRVMDI IHN LELKEPVFLKQSFN RTNL---YEV N KKT KNT---IFEICDA SGS1
 817 H DFRPDYKELKF KREYPDIPMIALTATA SEQRVMDI IHN LELKEPVFLKQSFN RTNL---YEV N KKT KNT---IFEICDA SGS1
 157 H DFRPEYA ALGQLRQRFPTLPFM ALTA ADDTTRQD IVRL LGLNDPLI QISSEDRPNIRY---MLMEKF KPLDQLM---RY recQ

* III IRKHHPYDSGIIYCLSRREC DT M ADTLQRDG L A ALAYHAGL SD SAR DEVQQKWINQDGQCIVICATIAFGMGIDKP DV RFV BLM
 882 INGRYKGQSGIIYCF SQKDSE QVTVSLQNLGIHAGAYHAN LEPE DKTTVHRK W SANE---IQV VVATVA FGMGIDKP DV RFV REQL
 230 VKSRFKNQQTGIIYCHSKKSCEQ TSQAQMQRNGIKCAYYHAGME PDERILSVQKA W QADE---IQV ICATVA FGMGIDKP DV RFV SGS1
 893 VQE Q-RGKSGIIYCN SRAKVEDTA ALQS KG ISAAAYHAGL ENNVRADVQEKFQRDD-LQIVVATVA FGMGINKP NVRFV recQ
 233

* IV IRKHHPYDSGIIYCLSRREC DT M ADTLQRDG L A ALAYHAGL SD SAR DEVQQKWINQDGQCIVICATIAFGMGIDKP DV RFV BLM
 882 INGRYKGQSGIIYCF SQKDSE QVTVSLQNLGIHAGAYHAN LEPE DKTTVHRK W SANE---IQV VVATVA FGMGIDKP DV RFV REQL
 230 VKSRFKNQQTGIIYCHSKKSCEQ TSQAQMQRNGIKCAYYHAGME PDERILSVQKA W QADE---IQV ICATVA FGMGIDKP DV RFV SGS1
 893 VQE Q-RGKSGIIYCN SRAKVEDTA ALQS KG ISAAAYHAGL ENNVRADVQEKFQRDD-LQIVVATVA FGMGINKP NVRFV recQ
 233

VI IHASLPKSVEGGYYQESGRAGR DGEISHCLLFYT YHDVTRLKRLIMMEKDGNHH TRETHFNNLYSMVHYCENITECRIQL BLM
 962 IHHSMSKSMENYYQESGRAGR DDMKADCILLYGGFDI FRISSMVVMENVGQQ---KLYEMVSYCQNISKSRRVLM REQL
 388 YHFTVPR TLLEGYYQETGRAGR DGNYSYCITYFSF RDDIRTMQTMIO KDKNLDRENKEKHLNKLQQVMA YCDN VTD CRRKLV SGS1
 972 VHFDIPRNIESYYQETGRAGR DGLPAEAMLFYDPA DMAWL RRCLEEKPQGQLQDIERH---KLNAMGAF AEQT-CRR LVL recQ
 311

FIG. 4

10 9 8 7 6 5 4 3 2 1 0

4.5 kb →

HG2162
HG2635
HeLa

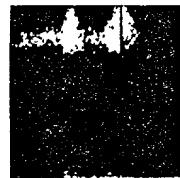


FIG. 5A

FIG. 5B

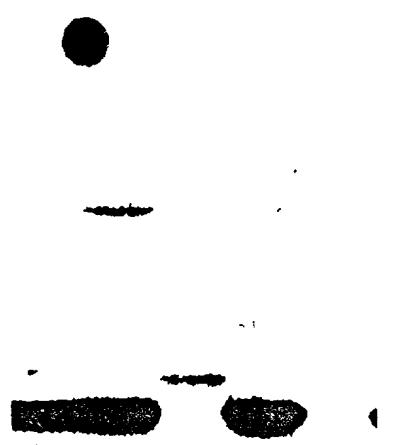


FIG. 6A



FIG. 6B

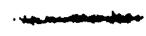


FIG. 6C

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FIG. 6D



FIG. 6E

